

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 10/051,643**ENTERED**CRF Processing Date: 2/12/2002Edited by: MC (STIC staff)Verified by: MC (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line. #2
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 203- corrected amino acid numbering

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



OIPE

RAW SEQUENCE LISTING

DATE: 02/12/2002

PATENT APPLICATION: US/10/051,643

TIME: 18:41:39

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\02122002\J051643.raw

P.S.

4 <110> APPLICANT: Watson, James D.
 5 Tan, Paul L. J.
 7 <120> TITLE OF INVENTION: Methods and Compounds for the Treatment
 8 of Immunologically-Mediated Diseases of the Respiratory
 9 System using Mycobacterium Vaccae
 12 <130> FILE REFERENCE: 11000.1008c2
 14 <140> CURRENT APPLICATION NUMBER: US/10/051,643
 14 <141> CURRENT FILING DATE: 2002-01-18
 14 <150> PRIOR APPLICATION NUMBER: US09/156,181
 15 <151> PRIOR FILING DATE: 1998-09-17
 17 <150> PRIOR APPLICATION NUMBER: US 08/996,624
 18 <151> PRIOR FILING DATE: 1997-12-23
 20 <160> NUMBER OF SEQ ID NOS: 208
 22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 25
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Mycobacterium vaccae
 29 <220> FEATURE:
 30 <221> NAME/KEY: UNSURE
 31 <222> LOCATION: (7)...(7)
 33 <400> SEQUENCE: 1
 34 Ala Pro Val Gly Pro Gly Xaa Ala Ala Tyr Val Gln Gln Val Pro Asp
 35 1 5 10 15
 36 Gly Pro Gly Ser Val Gln Gly Met Ala
 37 20 25
 39 <210> SEQ ID NO: 2
 40 <211> LENGTH: 10
 41 <212> TYPE: PRT
 42 <213> ORGANISM: Mycobacterium vaccae
 44 <220> FEATURE:
 45 <221> NAME/KEY: UNSURE
 46 <222> LOCATION: (2)...(2)
 48 <400> SEQUENCE: 2
 49 Met Xaa Asp Gln Leu Lys Val Asn Asp Asp
 50 1 5 10
 52 <210> SEQ ID NO: 3
 53 <211> LENGTH: 11
 54 <212> TYPE: PRT
 55 <213> ORGANISM: Mycobacterium vaccae
 57 <220> FEATURE:
 58 <221> NAME/KEY: UNSURE
 59 <222> LOCATION: (2)...(2)

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61 <400> SEQUENCE: 3
 OK 62 Met Xaa Pro Val Pro Val Ala Thr Ala Ala Tyr
 63 1 5 10
 65 <210> SEQ ID NO: 4
 66 <211> LENGTH: 21
 67 <212> TYPE: PRT
 68 <213> ORGANISM: Mycobacterium vaccae
 70 <400> SEQUENCE: 4
 71 Thr Pro Ala Pro Ala Pro Pro Tyr Val Asp His Val Glu Gln Ala
 72 1 5 10 15
 73 Lys Phe Gly Asp Leu
 74 20
 76 <210> SEQ ID NO: 5
 77 <211> LENGTH: 29
 78 <212> TYPE: PRT
 79 <213> ORGANISM: Mycobacterium vaccae
 81 <220> FEATURE:
 82 <221> NAME/KEY: UNSURE
 83 <222> LOCATION: (25)...(25)
 85 <400> SEQUENCE: 5
 86 Met Gln Ala Phe Asn Ala Asp Ala Tyr Ala Phe Ala Lys Arg Glu Lys
 87 1 5 10 15
 OK 88 Val Ser Leu Ala Pro Gly Val Pro Xaa Val Phe Glu Thr
 89 20 25
 91 <210> SEQ ID NO: 6
 92 <211> LENGTH: 21
 93 <212> TYPE: PRT
 94 <213> ORGANISM: Mycobacterium vaccae
 96 <220> FEATURE:
 97 <221> NAME/KEY: UNSURE
 98 <222> LOCATION: (6)...(6)
 OK 100 <400> SEQUENCE: 6
 101 Met Ala Asp Pro Asn Xaa Ala Ile Leu Gln Val Ser Lys Thr Thr Arg
 102 1 5 10 15
 103 Gly Gly Gln Ala Ala
 104 20
 106 <210> SEQ ID NO: 7
 107 <211> LENGTH: 11
 108 <212> TYPE: PRT
 109 <213> ORGANISM: Mycobacterium vaccae
 111 <400> SEQUENCE: 7
 112 Met Pro Ile Leu Gln Val Ser Gln Thr Gly Arg
 113 1 5 10
 115 <210> SEQ ID NO: 8
 116 <211> LENGTH: 14
 117 <212> TYPE: PRT
 118 <213> ORGANISM: Mycobacterium vaccae
 120 <220> FEATURE:
 121 <221> NAME/KEY: UNSURE

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122 <222> LOCATION: (2)...(2)

124 <221> NAME/KEY: UNSURE

125 <222> LOCATION: (6)...(6)

127 <400> SEQUENCE: 8

OK 128 Met Xaa Asp Pro Ile Xaa Leu Gln Leu Gln Val Ser Ser Thr

129 1 5 10

131 <210> SEQ ID NO: 9

132 <211> LENGTH: 16

133 <212> TYPE: PRT

134 <213> ORGANISM: Mycobacterium vaccae

136 <400> SEQUENCE: 9

137 Lys Ala Thr Tyr Val Gln Gly Gly Leu Gly Arg Ile Glu Ala Arg Val

138 1 5 10 15

140 <210> SEQ ID NO: 10

141 <211> LENGTH: 9

142 <212> TYPE: PRT

143 <213> ORGANISM: Mycobacterium vaccae

145 <220> FEATURE:

146 <221> NAME/KEY: UNSURE

147 <222> LOCATION: (2)...(2)

149 <400> SEQUENCE: 10

OK 150 Lys Xaa Gly Leu Ala Asp Leu Ala Pro

151 1 5

153 <210> SEQ ID NO: 11

154 <211> LENGTH: 14

155 <212> TYPE: PRT

156 <213> ORGANISM: Mycobacterium vaccae

158 <220> FEATURE:

159 <221> NAME/KEY: UNSURE

160 <222> LOCATION: (12)...(12)

161 <223> OTHER INFORMATION: Residue can be either Glu or Ile

163 <221> NAME/KEY: UNSURE

164 <222> LOCATION: (2)...(2)

166 <400> SEQUENCE: 11

OK 167 Lys Xaa Tyr Ala Leu Ala Leu Met Ser Ala Val Xaa Ala Ala

168 1 5 10

170 <210> SEQ ID NO: 12

171 <211> LENGTH: 11

172 <212> TYPE: PRT

173 <213> ORGANISM: Mycobacterium vaccae

175 <220> FEATURE:

176 <221> NAME/KEY: UNSURE

177 <222> LOCATION: (10)...(10)

179 <400> SEQUENCE: 12

OK 180 Lys Asn Pro Gln Val Ser Asp Glu Leu Xaa Thr

181 1 5 10

183 <210> SEQ ID NO: 13

184 <211> LENGTH: 21

185 <212> TYPE: PRT

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186 <213> ORGANISM: Mycobacterium vaccae

188 <220> FEATURE:

189 <221> NAME/KEY: UNSURE

190 <222> LOCATION: (9)...(9)

192 <400> SEQUENCE: 13

193 Ala Pro Ala Pro Ala Ala Pro Ala Xaa Gly Asp Pro Ala Ala Val Val

194 1 5 10 15

195 Ala Ala Met Ser Thr

196 20

198 <210> SEQ ID NO: 14

199 <211> LENGTH: 15

200 <212> TYPE: PRT

201 <213> ORGANISM: Mycobacterium vaccae

203 <220> FEATURE:

204 <221> NAME/KEY: UNSURE

205 <222> LOCATION: (5)...(5)

207 <400> SEQUENCE: 14

208 Glu Ala Glu Val Xaa Tyr Leu Gly Gln Pro Gly Glu Leu Val Asn

209 1 5 10 15

211 <210> SEQ ID NO: 15

212 <211> LENGTH: 15

213 <212> TYPE: PRT

214 <213> ORGANISM: Mycobacterium vaccae

216 <220> FEATURE:

217 <221> NAME/KEY: UNSURE

218 <222> LOCATION: (2)...(2)

219 <223> OTHER INFORMATION: Residue can be either Gly or Ala

221 <221> NAME/KEY: UNSURE

222 <222> LOCATION: (15)...(15)

223 <223> OTHER INFORMATION: Residue can be either Pro or Ala

225 <221> NAME/KEY: UNSURE

226 <222> LOCATION: (7)...(7)

228 <400> SEQUENCE: 15

229 Ala Xaa Val Val Pro Pro Xaa Gly Pro Pro Ala Pro Gly Ala Xaa

230 1 5 10 15

232 <210> SEQ ID NO: 16

233 <211> LENGTH: 15

234 <212> TYPE: PRT

235 <213> ORGANISM: Mycobacterium vaccae

237 <400> SEQUENCE: 16

238 Ala Pro Ala Pro Asp Leu Gln Gly Pro Leu Val Ser Thr Leu Ser

239 1 5 10 15

241 <210> SEQ ID NO: 17

242 <211> LENGTH: 25

243 <212> TYPE: PRT

244 <213> ORGANISM: Mycobacterium vaccae

246 <400> SEQUENCE: 17

247 Ala Thr Pro Asp Trp Ser Gly Arg Tyr Thr Val Val Thr Phe Ala Ser

248 1 5 10 15

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\02122002\J051643.raw

249 Asp Lys Leu Gly Thr Ser Val Ala Ala
 250 20 25
 252 <210> SEQ ID NO: 18
 253 <211> LENGTH: 25
 254 <212> TYPE: PRT
 255 <213> ORGANISM: Mycobacterium vaccae
 257 <220> FEATURE:
 258 <221> NAME/KEY: UNSURE
 259 <222> LOCATION: (15)...(15)
 260 <223> OTHER INFORMATION: Residue can be either Ala or Arg
 262 <221> NAME/KEY: UNSURE
 263 <222> LOCATION: (23)...(23)
 264 <223> OTHER INFORMATION: Residue can be either Val or Leu
 266 <221> NAME/KEY: UNSURE
 267 <222> LOCATION: (16)...(16)
 269 <400> SEQUENCE: 18
 W--> 270 Ala Pro Pro Tyr Asp Asp Arg Gly Tyr Val Asp Ser Thr Ala Xaa Xaa
 271 1 5 10 15
 W--> 272 Ala Ser Pro Pro Thr Leu Xaa Val Val
 273 20 25
 275 <210> SEQ ID NO: 19
 276 <211> LENGTH: 8
 277 <212> TYPE: PRT
 278 <213> ORGANISM: Mycobacterium vaccae
 280 <400> SEQUENCE: 19
 281 Glu Pro Glu Gly Val Ala Pro Pro
 282 1 5
 284 <210> SEQ ID NO: 20
 285 <211> LENGTH: 25
 286 <212> TYPE: PRT
 287 <213> ORGANISM: Mycobacterium vaccae
 289 <220> FEATURE:
 290 <221> NAME/KEY: UNSURE
 291 <222> LOCATION: (21)...(22)
 293 <400> SEQUENCE: 20
 294 Glu Pro Ala Gly Ile Pro Ala Gly Phe Pro Asp Val Ser Ala Tyr Ala
 295 1 5 10 15
 W--> 296 Ala Val Asp Pro Xaa Xaa Tyr Val Val
 297 20 25
 299 <210> SEQ ID NO: 21
 300 <211> LENGTH: 15
 301 <212> TYPE: PRT
 302 <213> ORGANISM: Mycobacterium vaccae
 304 <220> FEATURE:
 305 <221> NAME/KEY: UNSURE
 306 <222> LOCATION: (7)...(7)
 308 <400> SEQUENCE: 21
 W--> 309 Ala Pro Val Gly Pro Gly Xaa Ala Ala Tyr Val Gln Gln Val Pro
 310 1 5 10 15

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\PTO.AMC.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:49 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:62 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:88 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:88 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:101 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:128 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:150 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:180 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:193 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:208 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:296 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:309 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:351 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1369 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:63
L:1369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1371 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:63
L:1371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1386 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:64
L:1386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:1405 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:65
L:1405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:1407 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:65

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L:1407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:1526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:2095 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101
L:2108 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:102
L:2108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102
L:2129 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:103
L:2129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103
L:2131 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:103
L:2131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103
L:2153 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:105
L:2153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:105
L:2192 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:107
L:2192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:107
L:2266 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:111
L:2266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:111
L:2295 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:112
L:2295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:112
L:2572 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:120
L:2572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120
L:2573 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:120
L:2573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120
L:2632 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:121
L:2632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:121
L:2634 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:121
L:2634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:121
L:2948 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:134
L:2948 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134
L:3016 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:136
L:3016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:136
L:3035 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:137
L:3035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137
L:3048 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:138
L:3048 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138
L:3082 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:140
L:3082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140
L:3189 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:146
L:3189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146
L:3256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:148
L:3279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:149
L:3364 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:153
L:3403 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:154
L:3965 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:171
L:3966 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:171
L:4026 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:172
L:4028 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:172
L:4286 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:177
L:4566 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:185
L:4567 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:185
L:4607 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:186

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L:4634 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:187
L:4687 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:191
L:4704 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:192
L:5053 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:203